

CIBT-P01-130 Sequence Listing
SEQUENCE LISTING

<110> Huston, J.
Houston, L.L.
Ring, D.
Oppermann, H.

<120> BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING

<130> CIBT-P01-130

<140> 09/558,741
<141> 2000-04-26

<150> 07/831,967
<151> 1992-02-06

<160> 16

<170> PatentIn version 3.1

<210> 1
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> 741F8 sFv'

<220>
<221> CDS
<222> (3)..(752)
<223>

<400> 1

cc atg	gcg	gag	atc	caa	ttg	gtg	cag	tct	gga	cct	gag	ctg	aag	aag	1	5	10	15	47
Met	Ala	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys					

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc

Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	20	25	30	95
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	----

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta

Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	143
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	-----

aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct

Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Asn	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	50	55	60	191
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	-----

gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc

Glu	Glu	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Ser	65	70	75	239
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	-----

act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca

Thr	Ala	Tyr	Leu	Gln	Ile	Lys	Lys	Leu	Lys	Asn	Glu	Asp	Thr	Ala	Thr	80	85	90	95	287
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	----	-----

tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg

Page	1	335
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CIBT-P01-130SequenceListing

Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp			
100	105	110	
ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct			383
Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser			
115	120	125	
tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct			431
Ser Ser Gly Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro			
130	135	140	
aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag			479
Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys			
145	150	155	
gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca			527
Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro			
160	165	170	175
ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act			575
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr			
180	185	190	
gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act			623
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr			
195	200	205	
ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt			671
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys			
210	215	220	
cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg			719
Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Thr Lys Leu			
225	230	235	
gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt			772
Glu Ile Lys Arg Ala Asp Gly Gly Gly Cys			
240	245	250	
gggtctcggtt acgttgcgga tctcgaggct atctttacta actcttaccg taaagttctg			832
gctcaactgt ctgcacgcaa gctttgcag gatatcatga gcgcctaaga tccgtcgacc			892
tgcaggcatg caagctt			909

<210> 2
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> 741F8 sFv'

<400> 2

Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
1 5 10 15

Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

CIBT-P01-130SequenceListing

Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
35 40 45

Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
50 55 60

Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
65 70 75 80

Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr
85 90 95

Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
115 120 125

Ser Ser Gly Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
130 135 140

Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
145 150 155 160

Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
180 185 190

Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
195 200 205

Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
210 215 220

Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys Arg Ala Asp Gly Gly Gly Cys
245 250

<210> 3
<211> 779
<212> DNA
<213> Artificial Sequence

CIBT-P01-130 Sequence Listing

<220>
<223> 26-10 sFV'
<220>
<221> CDS
<222> (3)..(758)
<223>

<400> 3		
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1 5 10 15		
ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc	95	
Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr		
20 25 30		
gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac	143	
Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp		
35 40 45		
tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag	191	
Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln		
50 55 60		
aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act	239	
Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr		
65 70 75		
gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac	287	
Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr		
80 85 90 95		
tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt	335	
Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly		
100 105 110		
cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt	383	
His Gly Ala Ser Val Thr Val Ser Ser Gly Ser Ser Ser Ser Gly		
115 120 125		
tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct	431	
Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser		
130 135 140		
ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc	479	
Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser		
145 150 155		
cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg	527	
Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu		
160 165 170 175		
caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac	575	
Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn		
180 185 190		
cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act	623	
Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr		
195 200 205		
gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc	671	
Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile		

CIBT-P01-130SequenceListing
210 215 220

tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly	719
225 230 235	
acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys	768
240 245 250	
ccggggggatc c	779

<210> 4
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-10 sFv'

<400> 4

Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
1 5 10 15

Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
20 25 30

Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
35 40 45

Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
85 90 95

Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
100 105 110

Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Gly Ser
115 120 125

Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
130 135 140

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
145 150 155 160

CIBT-P01-130 Sequence Listing

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
 165 170 175

Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
 210 215 220

Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
 225 230 235 240

Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Cys
 245 250

<210> 5
 <211> 739
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 520C9 sFv

<220>
 <221> CDS
 <222> (1)...(729)
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 Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat 96
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
 20 25 30

gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg 144
 Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc 192
 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
 50 55 60

aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat 240
 Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
 65 70 75 80

ttg cag atc aac aac ctc aga aat gag gac tcg gcc aca tat ttc tgt 288
 Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys

CIBT-P01-130 Sequence Listing

85	90	95	
gca aga cga ttt ggg ttt gct tac tgg ggc caa ggg act ctg gtc agt Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser 100 105 110			336
gtc tct gca tcg ata tcg agc tcc tcc gga tct tca tct agc ggt tcc Val Ser Ala Ser Ile Ser Ser Ser Gly Ser Ser Ser Gly Ser 115 120 125			384
agc tcg agt gga tcc gat atc cag atg acc cag tct cca tcc tcc tta Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu 130 135 140			432
tct gcc tct ctg gga gaa aga gtc agt ctc act tgt cgg gca agt cag Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln 145 150 155 160			480
gac att ggt aat agc tta acc tgg ctt cag cag gaa cca gat gga act Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr 165 170 175			528
att aaa cgc ctg atc tac gcc aca tcc agt tta gat tct ggt gtc ccc Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro 180 185 190			576
aaa agg ttc agt ggc agt cgg tct ggg tca gat tat tct ctc acc atc Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile 195 200 205			624
agt agc ctt gag tct gaa gat ttt gta gtc tat tac tgt cta caa tat Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr 210 215 220			672
gct att ttt ccg tac acg ttc gga ggg ggg acc aac ctg gaa ata aaa Ala Ile Phe Pro Tyr Thr Phe Gly Gly Thr Asn Leu Glu Ile Lys 225 230 235 240			720
cg ^G gct gct gat taatctgcag Arg Ala Asp			739

<210> 6
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> 520C9 sFv

<400> 6

Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
20 25 30

Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

CIBT-P01-130SequenceListing

Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
65 70 75 80

Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser
100 105 110

Val Ser Ala Ser Ile Ser Ser Ser Gly Ser Ser Ser Gly Ser
115 120 125

Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln
145 150 155 160

Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr
165 170 175

Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro
180 185 190

Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile
195 200 205

Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr
210 215 220

Ala Ile Phe Pro Tyr Thr Phe Gly Gly Thr Asn Leu Glu Ile Lys
225 230 235 240

Arg Ala Asp

<210> 7
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Linker 1

<400> 7

CIBT-P01-130 Sequence Listing

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 8
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 2

<400> 8

Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly
1 5 10 15

<210> 9
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail

<400> 9

Ser Cys
1

C
G
V
<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail

<400> 10

Gly Gly Gly Gly Cys
1 5

<210> 11
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal tail

<400> 11

His His His His His Gly Gly Gly Cys
1 5 10

<210> 12
<211> 118
<212> PRT
<213> Mus musculus

<400> 12

CIBT-P01-130SequenceListing

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Glu Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe
65 70 75 80

Asn Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser Lys
115

C
<210> 13
<211> 120
<212> PRT
<213> Mus musculus

<400> 13

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp Phe
20 25 30

Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr Ile
35 40 45

Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

CIBT-P01-130SequenceListing

Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His Gly
100 105 110

Ala Ala Ser Val Thr Val Ser Ser
115 120

<210> 14
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> Hybrid peptide

<400> 14

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Leu Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Cys Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly His Gly Ala Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 15
<211> 103
<212> PRT
<213> Artificial sequence

<220>
<223> Hybrid peptide

<400> 15

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

CIBT-P01-130SequenceListing

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Leu Lys Gln Pro Pro Gly Arg Leu Glu Trp Ile Gly
35 40 45

Trp Ile Tyr Pro Gly Asn Gln Asn Thr Lys Tyr Asn Glu Asn Phe Lys
50 55 60

Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Tyr Thr His Tyr Tyr Phe
100

<210> 16

<211> 118

<212> PRT

<213> Mus musculus

<400> 16

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Ser Asn Asp
20 25 30

Tyr Tyr Thr Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Val Phe Tyr His Gly Thr Ser Asp Asp Thr Thr Pro Leu Arg
50 55 60

Ser Arg Val Thr Met Leu Val Asp Thr Ser Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Leu Ile Ala Gly Cys Ile Asp Val Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Ser
115

AUG-08-2002 16:10

ROPES & GRAY

P.19

CIBT-P01-130SequenceListing

Page 13